

## **STIC Biotechnology Systems Branch**

### **RAW SEQUENCE LISTING** **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/559,434  
Source: PCT 10  
Date Processed by STIC: 12/16/2005

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.2.2 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

**<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>**

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (**<<http://www.uspto.gov/efc/efs/downloads/documents.htm>>** , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):  
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

## Raw Sequence Listing Error Summary

## ERROR DETECTED

### SUGGESTED CORRECTION

**SERIAL NUMBER:**

$$\underline{10} \overline{) 559,434}$$

**ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE**

- 1** \_\_\_\_\_ Wrapped Nucleics  
          Wrapped Aminos      The number/text at the end of each line “wrapped” down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent “wrapping.”
- 2** \_\_\_\_\_ Invalid Line Length      The rules require that a line **not exceed** 72 characters in length. This includes white spaces.
- 3** \_\_\_\_\_ Misaligned Amino  
          Numbering      The numbering under each 5<sup>th</sup> amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.
- 4** \_\_\_\_\_ Non-ASCII      The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**
- 5** \_\_\_\_\_ Variable Length      Sequence(s)\_\_\_\_\_ contain n’s or Xaa’s representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6** \_\_\_\_\_ PatentIn 2.0  
          “bug”      A “bug” in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) \_\_\_\_\_. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
- 7** \_\_\_\_\_ Skipped Sequences  
          (OLD RULES)      Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for **each** skipped sequence:  
                                (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where “X” is shown)  
                                (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
                                (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where “X” is shown)  
                                This sequence is intentionally skipped
- Please also adjust the “(ii) NUMBER OF SEQUENCES:” response to **include** the skipped sequences.
- 8** \_\_\_\_\_ Skipped Sequences  
          (NEW RULES)      Sequence(s) \_\_\_\_\_ missing. If **intentional**, please insert the following lines for **each** skipped sequence.  
                                <210> sequence id number  
                                <400> sequence id number  
                                000
- 9** \_\_\_\_\_ Use of n’s or Xaa’s  
          (NEW RULES)      Use of n’s and/or Xaa’s have been detected in the Sequence Listing.  
                                Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n’s or Xaa’s are present.  
                                In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.
- 10** \_\_\_\_\_ Invalid <213>  
               Response      Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence
- 11** \_\_\_\_\_ Use of <220>      ~~Sequence(s) \_\_\_\_\_ missing the <220> “Feature” and associated numeric identifiers and responses.~~  
Use of <220> to <223> is MANDATORY if <213> “Organism” response is “Artificial Sequence” or “Unknown.” Please explain source of genetic material in <220> to <223> section.  
(See “Federal Register,” 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12** \_\_\_\_\_ PatentIn 2.0  
          “bug”      Please do not use “Copy to Disk” function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use “File Manager” or any other manual means to copy file to floppy disk.
- 13** \_\_\_\_\_ Misuse of n/Xaa      “n” can **only** represent a single nucleotide; “Xaa” can **only** represent a single amino acid



IFWP

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/559,434

DATE: 12/16/2005

TIME: 15:38:57

Input Set : A:\SEQUENCE LISTING.txt

Output Set : N:\CRF4\12162005\J559434.raw

3 <110> APPLICANT: Degussa AG  
 5 <120> TITLE OF INVENTION: Screening process for hydantoin racemases  
 7 <130> FILE REFERENCE: 030115 AM  
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/559,434  
 C--> 10 <141> CURRENT FILING DATE: 2005-12-05  
 12 <160> NUMBER OF SEQ ID NOS: 16  
 14 <170> SOFTWARE: PatentIn Ver. 2.1

Does Not Comply  
 Corrected Diskette Needed  
 Cp9-1,2,3,4,5

## ERRORED SEQUENCES

156 <210> SEQ ID NO: 4  
 157 <211> LENGTH: 237 → found 236  
 158 <212> TYPE: PRT  
 159 <213> ORGANISM: Artificial sequence  
 W--> 160  
 160 <223> OTHER INFORMATION: Description of the artificial sequence (1BG7)  
 162 <400> SEQUENCE: 4  
 163 Met Arg Ile Leu Val Ile Asn Pro Asn Ser Ser Ser Ala Leu Thr Glu  
 164 1 5 10 15  
 166 Ser Val Ala Asp Ala Ala Gln Gln Val Val Ala Thr Gly Thr Ile Ile  
 167 20 25 30  
 169 Ser Ala Ile Asn Pro Ser Arg Gly Pro Ala Val Ile Glu Gly Ser Phe  
 170 35 40 45  
 172 Asp Glu Ala Leu Ala Thr Phe His Leu Ile Glu Glu Val Glu Arg Ala  
 173 50 55 60  
 175 Glu Arg Glu Asn Pro Pro Asp Ala Tyr Val Ile Ala Cys Phe Arg Asp  
 176 65 70 75 80  
 178 Pro Gly Leu Asp Ala Val Lys Glu Leu Thr Asp Arg Pro Val Val Gly  
 179 85 90 95  
 181 Val Ala Glu Ala Ala Ile His Met Ser Ser Phe Val Ala Ala Thr Phe  
 182 100 105 110  
 184 Ser Ile Val Ser Ile Leu Pro Arg Val Arg Lys His Leu His Glu Leu  
 185 115 120 125  
 187 Val Arg Gln Ala Gly Ala Thr Asn Arg Leu Ala Ser Ile Lys Leu Pro  
 188 130 135 140  
 190 Asn Leu Gly Val Met Ala Phe His Glu Asp Glu His Ala Ala Leu Glu  
 191 145 150 155 160  
 193 Thr Leu Lys Gln Ala Ala Lys Glu Ala Val Gln Glu Asp Gly Ala Glu  
 194 165 170 175  
 196 Ser Ile Val Leu Gly Cys Ala Gly Met Val Gly Phe Ala Arg Gln Leu  
 197 180 185 190  
 199 Ser Asp Glu Leu Gly Val Pro Val Ile Asp Pro Val Glu Ala Ala Cys

Invalid Response  
 What is the  
 Source of genetic  
 Material?  
 Pls See Item  
 # 11 on  
 Error Summary  
 Sheet.

<210> 1  
<211> 6  
<212> PRT  
<213> Artificial sequence

<220>  
<223> Description of the artificial sequence  
Consensus sequence

<400> 1  
Phe Xaa Asp Xaa Gly Leu  
1 5

Pls Explain 'Xaa' locations which  
residue they represents.  
See Error Explanation on page-6

PY1

The type of errors shown exist throughout  
the Sequence Listing. Please check subsequent  
sequences for similar errors.

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/559,434

DATE: 12/16/2005

TIME: 15:38:57

Input Set : A:\SEQUENCE LISTING.txt

Output Set : N:\CRF4\12162005\J559434.raw

```

200          195          200          205
202 Arg Val Ala Glu Ser Leu Val Ala Leu Gly Tyr Gln Thr Ser Lys Ala
203          210          215          220
205 Asn Ser Tyr Gln Lys Pro Thr Glu Lys Gln Tyr Leu
E--> 206 225          230          235
283 <210> SEQ ID NO: 6
284 <211> LENGTH: 237
285 <212> TYPE: PRT
286 <213> ORGANISM: Artificial sequence
W--> 287 <223> OTHER INFORMATION: Description of the artificial sequence: 3CH11
E--> 289 <400> SEQUENCE: 6
290 Met Arg Ile Leu Val Ile Asn Pro Asn Ser Ser Ser Ala Leu Thr Glu
291 1          5          10          15
293 Ser Val Ala Asp Ala Ala Gln Gln Val Val Ala Thr Gly Thr Ile Ile
294          20          25          30
296 Ser Ala Ile Asn Pro Ser Arg Gly Pro Ala Val Ile Glu Gly Ser Phe
297          35          40          45
299 Asp Glu Ala Leu Ala Thr Phe His Leu Ile Glu Glu Val Glu Arg Ala
300          50          55          60
302 Glu Arg Glu Asn Pro Pro Asp Ala Tyr Val Ile Ala Cys Phe Glu Asp
303 65          70          75          80
305 Pro Gly Leu Asp Ala Val Lys Glu Leu Thr Asp Arg Pro Val Val Gly
306          85          90          95
308 Val Ala Glu Ala Ala Ile His Met Ser Ser Phe Val Ala Ala Thr Phe
309          100          105          110
311 Ser Ile Val Ser Ile Leu Pro Arg Val Arg Lys His Leu His Glu Leu
312          115          120          125
314 Val Arg Gln Ala Gly Ala Thr Asn Arg Leu Ala Ser Ile Lys Leu Pro
315          130          135          140
317 Asn Leu Gly Val Met Ala Phe His Glu Asp Glu His Ala Ala Leu Glu
318 145          150          155          160
320 Thr Leu Lys Gln Ala Ala Lys Glu Ala Val Gln Glu Asp Gly Ala Glu
321          165          170          175
323 Ser Ile Val Leu Gly Cys Ala Gly Met Val Gly Phe Ala Arg Gln Leu
324          180          185          190
326 Ser Asp Glu Leu Gly Val Pro Val Ile Asp Pro Val Glu Ala Ala Cys
327          195          200          205
329 Arg Val Ala Glu Ser Leu Val Ala Leu Gly Tyr Gln Thr Ser Lys Ala
330          210          215          220
332 Asn Ser Tyr Gln Lys Pro Thr Glu Lys Gln Tyr Leu
E--> 333 225          230          235
412 <210> SEQ ID NO: 8
413 <211> LENGTH: 237
414 <212> TYPE: PRT
415 <213> ORGANISM: Artificial sequence
W--> 416 <223> OTHER INFORMATION: Description of the artificial sequence: AE3
E--> 418 <400> SEQUENCE: 8

```

found 236

Insert &lt;220&gt;

Some Error

pls Insert &lt;220&gt;

Some Error

## RAW SEQUENCE LISTING

DATE: 12/16/2005

PATENT APPLICATION: US/10/559,434

TIME: 15:38:57

Input Set : A:\SEQUENCE LISTING.txt

Output Set: N:\CRF4\12162005\J559434.raw

419 Met Arg Ile Leu Val Ile Asn Pro Asn Ser Ser Ser Ala Leu Thr Glu  
420 1 5 10 15  
422 Ser Val Ala Asp Ala Ala Gln Gln Val Val Ala Thr Gly Thr Ile Ile  
423 20 25 30  
425 Ser Ala Ile Asn Pro Ser Arg Gly Pro Ala Val Ile Glu Gly Ser Phe  
426 35 40 45  
428 Asp Glu Ala Leu Ala Thr Phe His Leu Ile Glu Glu Val Glu Arg Ala  
429 50 55 60  
431 Glu Arg Glu Asn Pro Pro Asp Ala Tyr Val Ile Ala Cys Phe Gln Asp  
432 65 70 75 80  
434 Pro Gly Leu Asp Ala Val Lys Glu Leu Thr Asp Arg Pro Val Val Gly  
435 85 90 95  
437 Val Ala Glu Ala Ala Ile His Met Ser Ser Phe Val Ala Ala Thr Phe  
438 100 105 110  
440 Ser Ile Val Ser Ile Leu Pro Arg Val Arg Lys His Leu His Glu Leu  
441 115 120 125  
443 Val Arg Gln Ala Gly Ala Thr Asn Arg Leu Ala Ser Ile Lys Leu Pro  
444 130 135 140  
446 Asn Leu Gly Val Met Ala Phe His Glu Asp Glu His Ala Ala Leu Glu  
447 145 150 155 160  
449 Thr Leu Lys Gln Ala Ala Lys Glu Ala Val Gln Glu Asp Gly Ala Glu  
450 165 170 175  
452 Ser Ile Val Leu Gly Cys Ala Gly Met Val Gly Phe Ala Arg Gln Leu  
453 180 185 190  
455 Ser Asp Glu Leu Gly Val Pro Val Ile Asp Pro Val Glu Ala Ala Cys  
456 195 200 205  
458 Arg Val Ala Glu Ser Leu Val Ala Leu Gly Tyr Gln Thr Ser Lys Ala  
459 210 215 220  
461 Asn Ser Tyr Gln Lys Pro Thr Glu Lys Gln Tyr Leu  
E--> 462 225 230 235  
541 <210> SEQ ID NO: 10  
542 <211> LENGTH: 237 → found 236  
543 <212> TYPE: PRI  
544 <213> ORGANISM: Artificial sequence  
W--> 545 : → <220> Insert  
545 <223> OTHER INFORMATION: Description of the artificial sequence: BB5  
E--> 547 <400> SEQUENCE: 10  
548 Met Arg Ile Leu Val Ile Asn Pro Asn Ser Ser Ser Ala Leu Thr Glu  
549 1 5 10 15  
551 Ser Val Ala Asp Ala Ala Gln Gln Val Val Ala Thr Gly Thr Ile Ile  
552 20 25 30  
554 Ser Ala Ile Asn Pro Ser Arg Gly Pro Ala Val Ile Glu Gly Ser Phe  
555 35 40 45  
557 Asp Glu Ala Leu Ala Thr Phe His Leu Ile Glu Glu Val Glu Arg Ala  
558 50 55 60  
560 Glu Arg Glu Asn Pro Pro Asp Ala Tyr Val Ile Ala Cys Phe Leu Asp  
561 65 70 75 80  
563 Pro Gly Leu Asp Ala Val Lys Glu Leu Thr Asp Arg Pro Val Val Gly  
564 85 90 95

Same error

The type of errors shown exist throughout  
the sequence listing. Please check subsequent  
sequences for similar errors.

## RAW SEQUENCE LISTING

DATE: 12/16/2005

PATENT APPLICATION: US/10/559,434

TIME: 15:38:57

Input Set : A:\SEQUENCE LISTING.txt

Output Set: N:\CRF4\12162005\J559434.raw

```
566 Val Ala Glu Ala Ala Ile His Met Ser Ser Phe Val Ala Ala Thr Phe
567          100          105          110
569 Ser Ile Val Ser Ile Leu Pro Arg Val Arg Lys His Leu His Glu Leu
570          115          120          125
572 Val Arg Gln Ala Gly Ala Thr Asn Arg Leu Ala Ser Ile Lys Leu Pro
573          130          135          140
575 Asn Leu Gly Val Met Ala Phe His Glu Asp Glu His Ala Ala Leu Glu
576 145          150          155          160
578 Thr Leu Lys Gln Ala Ala Lys Glu Ala Val Gln Glu Asp Gly Ala Glu
579          165          170          175
581 Ser Ile Val Leu Gly Cys Ala Gly Met Val Gly Phe Ala Arg Gln Leu
582          180          185          190
584 Ser Asp Glu Leu Gly Val Pro Val Ile Asp Pro Val Glu Ala Ala Cys
585          195          200          205
587 Arg Val Ala Glu Ser Leu Val Ala Leu Gly Tyr Gln Thr Ser Lys Ala
588          210          215          220
591 Asn Ser Tyr Gln Lys Pro Thr Glu Lys Gln Tyr Leu
E--> 592 225          230          235
```

## VARIABLE LOCATION SUMMARY

DATE: 12/16/2005

PATENT APPLICATION: US/10/559,434

TIME: 15:38:58

Input Set : A:\SEQUENCE LISTING.txt

Output Set: N:\CRF4\12162005\J559434.raw

Use of n's or Xaa's (NEW RULES):

Use of n's and/or Xaa's have been detected in the Sequence Listing.

Use of &lt;220&gt; to &lt;223&gt; is MANDATORY if n's or Xaa's are present.

in &lt;220&gt; to &lt;223&gt; section, please explain location of n or Xaa, and which residue n or Xaa represents.

Seq#:1; Xaa Pos. 2,4

Seq#:14; N Pos. 49

*Error Explanation*



## VERIFICATION SUMMARY

DATE: 12/16/2005

PATENT APPLICATION: US/10/559,434

TIME: 15:38:58

Input Set : A:\SEQUENCE LISTING.txt

Output Set: N:\CRF4\12162005\J559434.raw

L:9 M:270 C: Current Application Number differs, Replaced Application Number  
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:26 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:1  
L:26 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:1  
L:26 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0  
L:160 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:4  
L:162 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:4  
L:206 M:252 E: No. of Seq. differs, <211> LENGTH:Input:237 Found:236 SEQ:4  
L:287 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:6  
L:289 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:6  
L:333 M:252 E: No. of Seq. differs, <211> LENGTH:Input:237 Found:236 SEQ:6  
L:416 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:8  
L:418 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:8  
L:462 M:252 E: No. of Seq. differs, <211> LENGTH:Input:237 Found:236 SEQ:8  
L:545 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10  
L:547 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:10  
L:592 M:252 E: No. of Seq. differs, <211> LENGTH:Input:237 Found:236 SEQ:10  
L:832 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:14  
L:832 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:14  
L:832 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:0